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Application No: 10522106 Version No: 1.0

**Input Set:**

**Output Set:**

**Started:** 2007-08-21 07:56:35.977  
**Finished:** 2007-08-21 07:56:38.925  
**Elapsed:** 0 hr(s) 0 min(s) 2 sec(s) 948 ms  
**Total Warnings:** 2  
**Total Errors:** 0  
**No. of SeqIDs Defined:** 24  
**Actual SeqID Count:** 24

Error code	Error Description
W 213	Artificial or Unknown found in <213> in SEQ ID (23)
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## SEQUENCE LISTING

<110> Kogel, Karl-Heinz  
Huckelhoven, Ralph  
Trujillo, Marco

<120> Method for Obtaining the pathogenic resistance in plants

<130> 12810-00067-US

<140> 10522106

<141> 2007-08-21

<160> 24

<170> PatentIn version 3.3

<210> 1

<211> 337

<212> DNA

<213> Hordeum vulgare

<220>

<221> CDS

<222> (2)..(337)

<223> coding for NADPH oxidase (fragment)

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1                       5                       10                       15	
att gag atg cac aac tat ctc aca agt gtt tat gag gaa ggg gat gct	97
Ile Glu Met His Asn Tyr Leu Thr Ser Val Tyr Glu Glu Gly Asp Ala	
20                      25                      30	
cgg tca gca ctc atc aca atg ctg caa gct ctc aac cat gcc aag aat	145
Arg Ser Ala Leu Ile Thr Met Leu Gln Ala Leu Asn His Ala Lys Asn	
35                      40                      45	
ggt gtc gat gta gtg tct ggm act cga gtc cgg aca cat ttt gca aga	193
Gly Val Asp Val Val Ser Xaa Thr Arg Val Arg Thr His Phe Ala Arg	
50                      55                      60	
cca aat ttt aag agg gtg ctg tct aag gta gcc gcc aaa cat cct tat	241
Pro Asn Phe Lys Arg Val Leu Ser Lys Val Ala Ala Lys His Pro Tyr	
65                      70                      75                      80	
gcc aag ata gga gtg ttc tat tgc gga gct cca gtt ctg gcg cag gaa	289
Ala Lys Ile Gly Val Phe Tyr Cys Gly Ala Pro Val Leu Ala Gln Glu	
85                      90                      95	
cta agc aac ctt tgc cat gag ttc aat ggc aaa tgc acg aca aaa ttc	337
Leu Ser Asn Leu Cys His Glu Phe Asn Gly Lys Cys Thr Thr Lys Phe	
100                    105                    110	

<210> 2

<211> 112

<212> PRT

<213> Hordeum vulgare

<220>

<221> misc\_feature

<222> (55)..(55)

<223> The 'Xaa' at location 55 stands for Gly.

<400> 2

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Ile Glu Met His Asn Tyr Leu Thr Ser Val Tyr Glu Glu Gly Asp Ala  
20 25 30  
Arg Ser Ala Leu Ile Thr Met Leu Gln Ala Leu Asn His Ala Lys Asn  
35 40 45  
Gly Val Asp Val Val Ser Xaa Thr Arg Val Arg Thr His Phe Ala Arg  
50 55 60  
Pro Asn Phe Lys Arg Val Leu Ser Lys Val Ala Ala Lys His Pro Tyr  
65 70 75 80  
Ala Lys Ile Gly Val Phe Tyr Cys Gly Ala Pro Val Leu Ala Gln Glu  
85 90 95  
Leu Ser Asn Leu Cys His Glu Phe Asn Gly Lys Cys Thr Thr Lys Phe  
100 105 110

<210> 3

<211> 2832

<212> DNA

<213> Oryza sativa

<220>

<221> CDS

<222> (1)..(2829)

<223> coding for NADPH oxidase

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1 5 10 15  
acg aca ccg cgg tcg ctg acg acg ggc tcg tcg ccg cgc ggg tcc gac 96  
Thr Thr Pro Arg Ser Leu Ser Thr Gly Ser Ser Pro Arg Gly Ser Asp  
20 25 30  
gac cgg agc tcc gac gac ggg gag gag ctg gtc gag gtc acg ctc gac 144  
Asp Arg Ser Ser Asp Asp Gly Glu Glu Leu Val Glu Val Thr Leu Asp  
35 40 45  
ctg cag gac gac acc att gtg ctt cgg agc gtc gag ccc gcg gcg 192  
Leu Gln Asp Asp Asp Thr Ile Val Leu Arg Ser Val Glu Pro Ala Ala  
50 55 60  
gcg gcg gcg gcg ggg gtg ggg gcg ggg gcg ggg gcg gcg tcg gcg cgg 240  
Ala Ala Ala Ala Gly Val Gly Ala Gly Ala Ala Ser Ala Arg  
65 70 75 80  
ggg gag ctc acg ggt ggc ccg tcg tcg tcg tcg cgg tcg agg tcg 288  
Gly Glu Leu Thr Gly Gly Pro Ser Ser Ser Ser Arg Ser Arg Ser  
85 90 95  
ccg tcg atc cgg agg agc tcg tcg cac ccg ctg cag ttc tcg cag 336  
Pro Ser Ile Arg Arg Ser Ser Ser His Arg Leu Leu Gln Phe Ser Gln  
100 105 110  
gag ctc aag gcg gag gcc atg gcc ccg gcg ccg cag ttc tcg cag gac 384  
Glu Leu Lys Ala Glu Ala Met Ala Arg Ala Arg Gln Phe Ser Gln Asp  
115 120 125  
ctg acc aag cgg ttc ggc cgc agc cac agc cgc agc gaa gcg cag gcg 432  
Leu Thr Lys Arg Phe Gly Arg Ser His Ser Arg Ser Glu Ala Gln Ala  
130 135 140

ccg	ggc	ctc	gag	tcc	gcg	ctc	gcc	gcc	cgc	gcc	gca	cg	cgg	cgg	cag	480		
Pro	Ser	Gly	Leu	Glu	Ser	Ala	Leu	Ala	Ala	Arg	Ala	Ala	Arg	Arg	Gln			
145				150						155					160			
ccg	g	cg	c	tc	g	a	c	cg	tcc	ggc	gc	cac	a	ag	g	ctc	cg	528
Arg	Ala	Gln	Leu	Asp	Arg	Thr	Arg	Ser	Gly	Ala	His	Lys	Ala	Leu	Arg			
				165					170						175			
ggc	ctc	cgc	tcc	atc	agc	agc	aac	aag	gcc	aac	aac	gcc	tgg	atg	gag	576		
Gly	Leu	Arg	Phe	Ile	Ser	Ser	Asn	Lys	Ala	Asn	Asn	Ala	Trp	Met	Glu			
				180					185						190			
gtg	cag	gcc	aa	t	tc	gac	cg	cc	tc	g	cc	g	ac	tt	c	cc	624	
Val	Gln	Ala	Asn	Phe	Asp	Arg	Leu	Ala	Arg	Asp	Gly	Tyr	Leu	Ser	Arg			
				195					200						205			
tcc	gac	ttc	g	cc	gaa	tgc	atc	gg	atg	ac	gaa	tcg	a	ag	g	ag	ttc	672
Ser	Asp	Phe	Ala	Glu	Cys	Ile	Gly	Met	Thr	Glu	Ser	Lys	Glu	Phe	Ala			
				210					215						220			
ctc	gag	ct	ttc	gac	ac	ct	g	cg	cg	cg	ca	cag	at	g	tg	g	ac	720
Leu	Glu	Leu	Phe	Asp	Thr	Leu	Ser	Arg	Arg	Arg	Gln	Met	Lys	Val	Asp			
				225					230						235		240	
ac	att	aa	a	ag	gat	gaa	ctc	cg	gag	atc	tgg	cag	cag	atc	ac	c	at	768
Thr	Ile	Asn	Lys	Asp	Glu	Leu	Arg	Glu	Ile	Trp	Gln	Gln	Ile	Thr	Asp			
				245					250						255			
aa	ac	tc	g	ac	tcc	cgt	ctc	caa	atc	ttc	ttc	gaa	at	g	tg	g	at	816
Asn	Ser	Phe	Asp	Ser	Arg	Leu	Gln	Ile	Phe	Phe	Glu	Met	Val	Asp	Lys			
				260					265						270			
aa	ac	gc	g	gc	cg	att	ac	g	ag	g	cg	gt	aaa	g	ag	at	at	864
Asn	Ala	Asp	Gly	Arg	Ile	Thr	Glu	Ala	Glu	Val	Lys	Glu	Ile	Ile	Met			
				275					280						285			
tt	tg	ag	c	gc	t	ct	g	aa	at	g	tg	aaa	g	ag	at	at	at	912
Leu	Ser	Ala	Ser	Ala	Asn	Lys	Leu	Ser	Arg	Leu	Lys	Glu	Gln	Ala	Glu			
				290					295						300			
ga	g	ta	c	cc	tt	at	g	ag	g	ag	gt	aaa	g	ag	at	at	at	960
Glu	Tyr	Ala	Ala	Leu	Ile	Met	Glu	Glu	Leu	Asp	Pro	Glu	Gly	Leu	Gly			
				305					310						315		320	
ta	at	g	ag	ct	ta	tgg	ca	tt	g	ag	aca	ctt	ct	tg	t	gg	c	1008
Tyr	Ile	Glu	Leu	Trp	Gln	Leu	Glu	Thr	Leu	Leu	Gln	Lys	Asp	Thr				
				325					330						335			
ta	at	g	ac	ta	t	at	g	cc	tt	at	g	cc	ca	g	ca	ct	ag	1056
Tyr	Met	Asn	Tyr	Ser	Gln	Ala	Leu	Ser	Tyr	Thr	Ser	Gln	Ala	Leu	Ser			
				340					345						350			
ca	aa	t	tt	gca	gg	ct	ta	agg	aa	ag	at	tca	atc	cg	aaa	at	ac	1104
Gln	Asn	Leu	Ala	Gly	Leu	Arg	Lys	Lys	Ser	Ser	Ile	Arg	Lys	Ile	Ser			
				355					360						365			
ac	t	c	t	ta	ag	ca	t	tt	g	ag	ac	tgg	aa	cg	t	ta	tgg	1152
Thr	Ser	Leu	Ser	Tyr	Tyr	Phe	Glu	Asp	Asn	Trp	Lys	Arg	Leu	Trp	Val			
				370					375						380			
ct	tg	tg	tg	tt	gg	at	at	g	ct	gg	ttc	acc	tgg	aa	tt	c	1200	
Leu	Ala	Leu	Trp	Ile	Gly	Ile	Met	Ala	Gly	Leu	Phe	Thr	Trp	Lys	Phe			
				385					390						395		400	
at	cg	at	cgt	aa	cga	ta	t	gtc	ttt	gat	gt	at	gg	c	tac	tgt	gtc	1248
Met	Gln	Tyr	Arg	Asn	Arg	Tyr	Val	Phe	Asp	Val	Met	Gly	Tyr	Cys	Val			
				405					410						415			
ac	ac	ac	aa	gg	g	ct	g	ct	aa	at	at	g	ca	at			1296	
Thr	Thr	Ala	Lys	Gly	Ala	Ala	Glu	Thr	Leu	Lys	Leu	Asn	Met	Ala	Ile			
				420					425						430			
at	ct	ct	cc	gt	tg	cgt	aa	c	ac	at	act	tgg	tt	cg	ag	at	ca	1344
Ile	Leu	Leu	Pro	Val	Cys	Arg	Asn	Thr	Ile	Thr	Trp	Leu	Arg	Ser	Thr			
				435					440						445			

agg gct gca cg	gca cta cct ttt gat gac aac atc aac ttc cac aag	1392
Arg Ala Ala Arg Ala Leu Pro Phe Asp Asp Asn Ile Asn Phe His Lys		
450	455	460
act att gca gca gca att gtg gtt ggt ata atc ctc cat gca ggg aac	1440	
Thr Ile Ala Ala Ala Ile Val Val Gly Ile Ile Leu His Ala Gly Asn		
465	470	475
480		
cac ctt gta tgc gat ttt cca cgg tta ata aaa tca tca gat gag aag	1488	
His Leu Val Cys Asp Phe Pro Arg Leu Ile Lys Ser Ser Asp Glu Lys		
485	490	495
tat gct cct ttg ggc cag tat ttt ggg gaa ata aag cca aca tat ttt	1536	
Tyr Ala Pro Leu Gly Gln Tyr Phe Gly Glu Ile Lys Pro Thr Tyr Phe		
500	505	510
aca ttg gtc aaa gga gtg gag ggc atc act ggg gta atc atg gtt gta	1584	
Thr Leu Val Lys Gly Val Glu Gly Ile Thr Gly Val Ile Met Val Val		
515	520	525
tgc atg ata att gct ttt act cta gca acc cgg tgg ttc cgc cgt agc	1632	
Cys Met Ile Ile Ala Phe Thr Leu Ala Thr Arg Trp Phe Arg Arg Ser		
530	535	540
ttg gtt aag ctt cca agg cca ttt gac aaa ctg act ggc ttc aat gcc	1680	
Leu Val Lys Leu Pro Arg Pro Phe Asp Lys Leu Thr Gly Phe Asn Ala		
545	550	555
560		
ttt tgg tat tct cat cat ctg ttc atc att gtg tat atc gcg ctc att	1728	
Phe Trp Tyr Ser His His Leu Phe Ile Ile Val Tyr Ile Ala Leu Ile		
565	570	575
gtt cat gga gag tgt cta tac ctt att cat gtc tgg tac aga aga acg	1776	
Val His Gly Glu Cys Leu Tyr Leu Ile His Val Trp Tyr Arg Arg Thr		
580	585	590
aca tgg atg tat ctt tca gtg cct gtt tgc ttg tat gta ggg gag agg	1824	
Thr Trp Met Tyr Leu Ser Val Pro Val Cys Leu Tyr Val Gly Glu Arg		
595	600	605
att cta agg ttc ttc agg tct ggc agt tat tct gtc cgg cta ttg aag	1872	
Ile Leu Arg Phe Phe Arg Ser Gly Ser Tyr Ser Val Arg Leu Leu Lys		
610	615	620
gtg gcc ata tat cca ggt aat gtt ttg aca ctg caa atg tcc aag cct	1920	
Val Ala Ile Tyr Pro Gly Asn Val Leu Thr Leu Gln Met Ser Lys Pro		
625	630	635
640		
ccc acg ttc cgt tac aag agt gga caa tat atg ttt gtt caa tgt cca	1968	
Pro Thr Phe Arg Tyr Lys Ser Gly Gln Tyr Met Phe Val Gln Cys Pro		
645	650	655
gca gtg tct ccc ttt gaa tgg cat ccc ttc tca att act tca gca cct	2016	
Ala Val Ser Pro Phe Glu Trp His Pro Phe Ser Ile Thr Ser Ala Pro		
660	665	670
ggg gat gac tac ctc agc att cat gtt cga caa ctt ggt gat tgg aca	2064	
Gly Asp Asp Tyr Leu Ser Ile His Val Arg Gln Leu Gly Asp Trp Thr		
675	680	685
cga gaa ctc aag aga gta ttt gct gca gct tgt gag ccc cca gcg ggt	2112	
Arg Glu Leu Lys Arg Val Phe Ala Ala Ala Cys Glu Pro Pro Ala Gly		
690	695	700
ggt aaa agc ggc ctt ctt agg gca gat gag aca act aag aaa atc tta	2160	
Gly Lys Ser Gly Leu Leu Arg Ala Asp Glu Thr Thr Lys Lys Ile Leu		
705	710	715
720		
ccc aag ctt ctg att gat gga ccg tat ggt tct cct gct cag gat tac	2208	
Pro Lys Leu Leu Ile Asp Gly Pro Tyr Gly Ser Pro Ala Gln Asp Tyr		
725	730	735
agc aag tat gat gtt tta tta ctt gtt gga tta gga att ggt gcg aca	2256	
Ser Lys Tyr Asp Val Leu Leu Val Gly Leu Gly Ile Gly Ala Thr		
740	745	750

ccc ttt att agc ata tta aaa gat ctt ctg aat aac atc atc aaa atg		2304
Pro Phe Ile Ser Ile Leu Lys Asp Leu Leu Asn Asn Ile Ile Lys Met		
755	760	765
gag gaa gag gag gat gct tct act gat ctt tat cca cca atg ggt cggt		2352
Glu Glu Glu Asp Ala Ser Thr Asp Leu Tyr Pro Pro Met Gly Arg		
770	775	780
aat aag cca cat gtt gat ctg ggc aca ctt atg acg att acc tca aga		2400
Asn Lys Pro His Val Asp Leu Gly Thr Leu Met Thr Ile Thr Ser Arg		
785	790	795
800		
cca aag aag atc ttg aag acc aca aat gct tac ttt tac tgg gtc aca		2448
Pro Lys Lys Ile Leu Lys Thr Thr Asn Ala Tyr Phe Tyr Trp Val Thr		
805	810	815
cgt gag caa ggc tct ttt gat tgg ttc aaa gga gtc atg aat gaa att		2496
Arg Glu Gln Gly Ser Phe Asp Trp Phe Lys Gly Val Met Asn Glu Ile		
820	825	830
gct gac ttg gat caa agg aat atc att gag atg cac aac tac cta aca		2544
Ala Asp Leu Asp Gln Arg Asn Ile Ile Glu Met His Asn Tyr Leu Thr		
835	840	845
agc gtc tat gag gag ggg gat gcc agg tca gca ctc atc acc atg ctc		2592
Ser Val Tyr Glu Glu Gly Asp Ala Arg Ser Ala Leu Ile Thr Met Leu		
850	855	860
caa gct ctg aac cat gcc aag aat gga gtt gat att gtc tct ggg aca		2640
Gln Ala Leu Asn His Ala Lys Asn Gly Val Asp Ile Val Ser Gly Thr		
865	870	875
880		
aaa gtc cgg aca cat ttt gca cga cca aat tgg aga aag gtc ctt tct		2688
Lys Val Arg Thr His Phe Ala Arg Pro Asn Trp Arg Lys Val Leu Ser		
885	890	895
aaa att tcc tcc aag cat cca tat gcc aaa ata ggt gta ttc tac tgt		2736
Lys Ile Ser Ser Lys His Pro Tyr Ala Lys Ile Gly Val Phe Tyr Cys		
900	905	910
gga gct cca gtc ctg gca caa gaa cta agc aaa ctt tgc cat gaa ttc		2784
Gly Ala Pro Val Leu Ala Gln Glu Leu Ser Lys Leu Cys His Glu Phe		
915	920	925
aac ggg aaa tgc aca acg aag ttc gaa ttc cat aag gag cat ttc tga		2832
Asn Gly Lys Cys Thr Thr Lys Phe Glu Phe His Lys Glu His Phe		
930	935	940

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<211> 943  
<212> PRT  
<213> Oryza sativa

<400> 4

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Asp Arg Ser Ser Asp Asp Gly Glu Glu Leu Val Glu Val Thr Leu Asp		
35	40	45
Leu Gln Asp Asp Asp Thr Ile Val Leu Arg Ser Val Glu Pro Ala Ala		
50	55	60
Ala Ala Ala Ala Gly Val Gly Ala Gly Ala Gly Ala Ala Ser Ala Arg		
65	70	75
80		
Gly Glu Leu Thr Gly Gly Pro Ser Ser Ser Ser Arg Ser Arg Ser		
85	90	95
Pro Ser Ile Arg Arg Ser Ser Ser His Arg Leu Leu Gln Phe Ser Gln		
100	105	110

Glu Leu Lys Ala Glu Ala Met Ala Arg Ala Arg Gln Phe Ser Gln Asp  
115 120 125  
Leu Thr Lys Arg Phe Gly Arg Ser His Ser Arg Ser Glu Ala Gln Ala  
130 135 140  
Pro Ser Gly Leu Glu Ser Ala Leu Ala Ala Arg Ala Arg Arg Gln  
145 150 155 160  
Arg Ala Gln Leu Asp Arg Thr Arg Ser Gly Ala His Lys Ala Leu Arg  
165 170 175  
Gly Leu Arg Phe Ile Ser Ser Asn Lys Ala Asn Asn Ala Trp Met Glu  
180 185 190  
Val Gln Ala Asn Phe Asp Arg Leu Ala Arg Asp Gly Tyr Leu Ser Arg  
195 200 205  
Ser Asp Phe Ala Glu Cys Ile Gly Met Thr Glu Ser Lys Glu Phe Ala  
210 215 220  
Leu Glu Leu Phe Asp Thr Leu Ser Arg Arg Gln Met Lys Val Asp  
225 230 235 240  
Thr Ile Asn Lys Asp Glu Leu Arg Glu Ile Trp Gln Gln Ile Thr Asp  
245 250 255  
Asn Ser Phe Asp Ser Arg Leu Gln Ile Phe Phe Glu Met Val Asp Lys  
260 265 270  
Asn Ala Asp Gly Arg Ile Thr Glu Ala Glu Val Lys Glu Ile Ile Met  
275 280 285  
Leu Ser Ala Ser Ala Asn Lys Leu Ser Arg Leu Lys Glu Gln Ala Glu  
290